

Appendix A. Codes of layers of stress and correspondence of subtypes to major types

A.1. Codes of layers used in this work

Code	Type of stress
0	Hypoxia
1	Nutrient starvation
2	Cell wall damage
3	Ion deprivation
4	NO exposure
5	Generic oxidative stress
6	DNA damage

A.2. Correspondance of subtypes of stress to the major types of stress

Major type code	Subtype
0	Hypoxia
0	Reaireation
0	Wayne growth
1	Stationary phase
1	Nutrient starvation
1	Minimal medium
2	Surfactant
2	Spheroplast induced
2	NaCl
2	SDS
3	Phosphate
3	Iron scavengers
3	Iron
4	Deta NO
5	H ₂ O ₂
5	Diamide
6	UV

Appendix B. Dictionary of samples used in this work.

GEO series	Description	Strain	Stress	Subtype	Layer
GSE8839	merged MTB strain 1254 Ctrl vs 2hr Hypoxia	1254	Acontrol	Hypoxia	0
GSE21590	H37Rv 1hour reaeration	H37Rv	Respiration arrest	Reaireation	0
GSE21590	H37Rv 4hour reaeration	H37Rv	Respiration arrest	Reaireation	0
GSE21590	H37Rv 6hour reaeration	H37Rv	Respiration arrest	Reaireation	0
GSE21590	H37Rv 12hour reaeration	H37Rv	Respiration arrest	Reaireation	0
GSE21590	H37Rv 24hour reaeration	H37Rv	Respiration arrest	Reaireation	0
GSE8786	Growth curve 0 days Control	H37Rv	Acontrol	Wayne growth	0
GSE8786	Growth curve 6 days Control	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	Growth curve 8 days Control	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	Growth curve 14 days Control	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	Growth curve 24 days Control	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	Growth curve 60 days Control	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 4 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 6 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 8 days	H37Rv	Respiration	Wayne growth	0

			arrest		
GSE8786	oxygen-depleted Wayne Growth 10 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 12 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 14 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 20 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 30 days	H37Rv	Respiration arrest	Wayne growth	0
GSE8786	oxygen-depleted Wayne Growth 80 days	H37Rv	Respiration arrest	Wayne growth	0
GSE9331	H37Rv hypoxia 4hr	H37Rv	Respiration arrest	Hypoxia	0
GSE9331	H37Rv hypoxia 8hr	H37Rv	Respiration arrest	Hypoxia	0
GSE9331	H37Rv hypoxia 12hr	H37Rv	Respiration arrest	Hypoxia	0
GSE9331	H37Rv hypoxia 1day	H37Rv	Respiration arrest	Hypoxia	0
GSE9331	H37Rv hypoxia 4day	H37Rv	Respiration arrest	Hypoxia	0
GSE9331	H37Rv hypoxia 7day	H37Rv	Respiration arrest	Hypoxia	0
GSE8829	Hypoxic conditions experiment of M. tuberculosis wild type	H37Rv	Respiration arrest	Hypoxia	0
GSE1642	WT t=0h WT t=6h in TBST	H37Rv	Respiration arrest	Nutrient starvation	1
GSE1642	Minimal medium (Succinate) 7H9-based medium	H37Rv	Minimal medium	Minimal medium	1

GSE5977	Mtb late-log phase	H37Rv	Respiration arrest	Stationary phase	1
GSE5977	Mtb stationary phase	H37Rv	Respiration arrest	Stationary phase	1
GSE15976	H37Rv wild type Vs H37Rv wild type	H37Rv	Acontrol	SDS	2
GSE15976	H37Rv wild type control vs 0.05% SDS for 60 min	H37Rv	Cell wall damage	SDS	2
GSE6750	Rv-Control vs Rv-SDS treated	H37Rv	Cell wall damage	SDS	2
GSE8664	Exposed to 0.05% SDS H37Rv wild type	H37Rv	Cell wall damage	SDS	2
GSE50159	WT 140 mM NaCl	CDC1551	Cell wall damage	NaCl	2
GSE14840	24 hour phosphate starvation	CDC1551	Ion deprivation	Phosphate	3
GSE14840	72 hour phosphate starvation	CDC1551	Ion deprivation	Phosphate	3
GSE8732	inversion Comparison between iron-sufficient (50 uM FeCl ₃) and iron-deficient (2 uM FeCl ₃) grew conditions	H37Rv	Ion deprivation	Iron	3
GSE1642	100uM Dipyrldyl ctrl 6h	H37Rv	Ion deprivation	Iron scavengers	3
GSE1642	200uM Dipyrldyl ctrl 6h	H37Rv	Ion deprivation	Iron scavengers	3
GSE1642	150uM Deferoxamine ctrl 6h	H37Rv	Ion deprivation	Iron scavengers	3
GSE16146	MTB strain1254 vs MTB strain 1254 for DETA NO exp control	1254	Acontrol	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 0.005 mM DETA NO 40min	1254	Acontrol	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 0.05 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 0.5 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4

GSE16146	MTB strain 1254 Ctrl vs 1.0 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 5.0 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 0.5 mM DETA NO 4hrs	1254	Oxidative stress	DETA NO	4
GSE8839	merged H37Rv Ctrl vs 0,05 mM DETA NO 40min	H37Rv	Oxidative stress	DETA NO	4
GSE8839	merged CDC1551 Ctrl vs 0,05 mM DETA NO 40 min	CDC1551	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,05 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 1,0 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 5,0 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 5min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 20min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 40min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 1hr	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 2hrs	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 8hrs	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 16hrs	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 24hrs	1254	Oxidative stress	DETA NO	4

GSE8839	merged MTB strain 1254 Ctrl vs 0,5 mM DETA NO 24hrs + 0,5 mM DNO 40min	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs high aeration + 0,001 mM DETA NO	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs high aeration + 0,005 mM DETA NO	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs high aeration + 0,01 mM DETA NO	1254	Oxidative stress	DETA NO	4
GSE8839	merged MTB strain 1254 Ctrl vs high aeration + 0,05 mM DETA NO	1254	Oxidative stress	DETA NO	4
GSE16146	MTB strain 1254 Ctrl vs 0.05 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₄	5
GSE16146	MTB strain 1254 Ctrl vs 0.5 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₃	5
GSE16146	MTB strain 1254 Ctrl vs 5.0 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₂	5
GSE16146	MTB strain 1254 Ctrl vs 10.0 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₁	5
GSE16146	MTB strain 1254 Ctrl vs 50.0 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₀	5
GSE16146	MTB strain 1254 Ctrl vs 200 mM H2O2 40min	1254	Oxidative stress	H ₂ O ₁	5
GSE16146	MTB strain 1254 Ctrl vs 5.0 mM H2O2 4hr	1254	Oxidative stress	H ₂ O ₂	5
GSE8689	Exposed to Diamide 5 mM H37Rv wild type	H37Rv	Oxidative stress	Diamide	5
GSE15976	H37Rv wild type control vs 5mM Diamide for 60 min	H37Rv	Oxidative stress	Diamide	5
GSE1642	20mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE1642	20mJ cm2 UV ctrl (8h) H37Rv	H37Rv	DNA damage	UV	6
GSE1642	20mJ cm2 UV ctrl (12h) H37Rv	H37Rv	DNA damage	UV	6

GSE1642	25mJ cm2 UV ctrl (2h)	H37Rv	DNA damage	UV	6
GSE1642	25mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE1642	40mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE1642	40mJ cm2 UV ctrl (8h) H37Rv	H37Rv	DNA damage	UV	6
GSE1642	40mJ cm2 UV ctrl (12h) H37Rv	H37Rv	DNA damage	UV	6
GSE1642	60mJ cm2 UV ctrl (2h)	H37Rv	DNA damage	UV	6
GSE1642	60mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE365	20mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE365	20mJ cm2 UV ctrl (8h)	H37Rv	DNA damage	UV	6
GSE365	20mJ cm2 UV ctrl (12h)	H37Rv	DNA damage	UV	6
GSE365	25mJ cm2 UV ctrl (2h)	H37Rv	DNA damage	UV	6
GSE365	25mJ cm2 UV ctrl (4h)	H37Rv	DNA damage	UV	6
GSE365	25mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE365	40mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6
GSE365	40mJ cm2 UV ctrl (8h)	H37Rv	DNA damage	UV	6
GSE365	40mJ cm2 UV ctrl (12h)	H37Rv	DNA damage	UV	6
GSE365	60mJ cm2 UV ctrl (2h)	H37Rv	DNA damage	UV	6
GSE365	60mJ cm2 UV ctrl (4h)	H37Rv	DNA damage	UV	6
GSE365	60mJ cm2 UV ctrl (6h)	H37Rv	DNA damage	UV	6

Appendix C. Equivalent thresholds for different measures.

In this appendix, some parameters related to the pair of genes with highest FDR under the threshold are shown, as a measure of thresholds in other values (such as p-values or z-values). Codes of layers can be found in Appendix A. In gene differential coexpression, layers i and j are the ones used in equations 16 to 21.

C.1. For gene co-expression

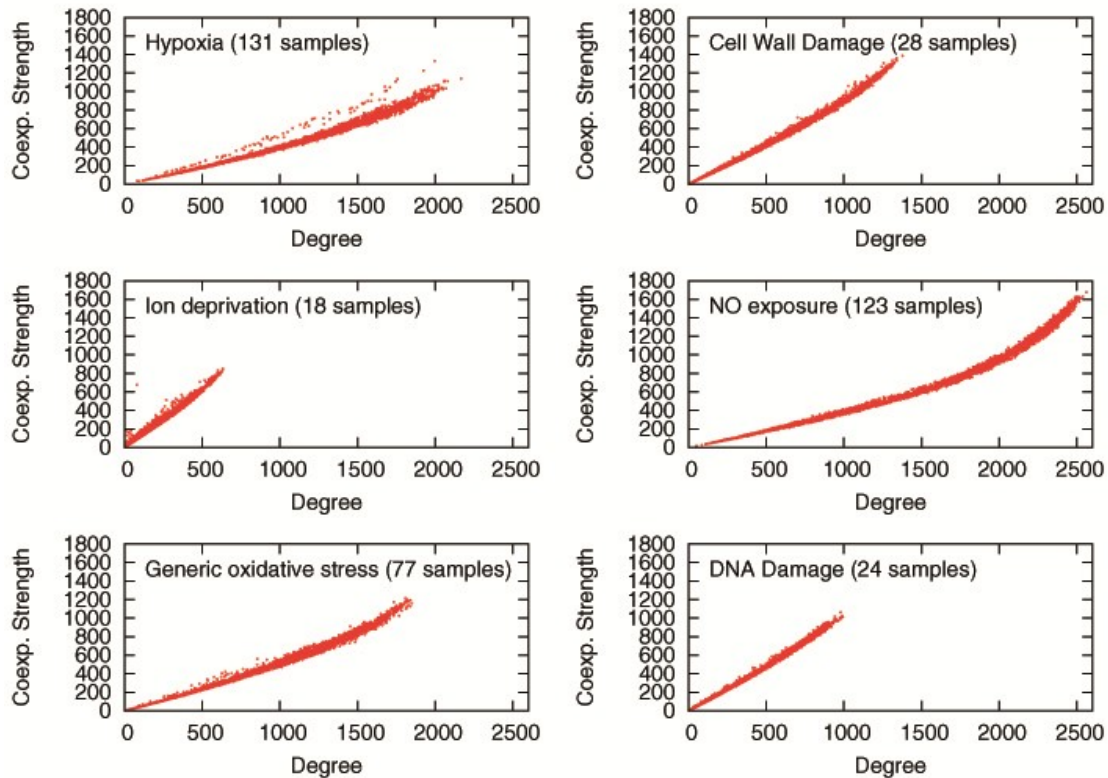
Layer	Highest fdr	Z-value	p-value
0	0.009999999	2.987183191	0.00281561
2	0.009999642	3.2569864	0.001126018
3	0.009998805	3.513362623	0.000442473
4	0.009999956	2.921602026	0.003482362
5	0.009999928	3.051222077	0.002279119
6	0.009995548	3.37179765	0.000746793

C.2. For gene differential co-expression

Layer i	Layer j	Highest fdr	Z-value	p-value
0	2	0.009999957	3.275032268	0.001056499
0	3	0.009999939	3.456757672	0.000546716
0	4	0.009999993	2.966311095	0.003013955
0	5	0.009999985	3.093276838	0.001979594
0	6	0.009999961	3.28158053	0.00103227
2	3	0.009999992	3.47318713	0.000514317
2	4	0.009999999	3.206360222	0.001344256
2	5	0.009999974	3.385355353	0.000710862
2	6	0.009999963	3.34286059	0.000829195
3	4	0.009999919	3.398168319	0.000678387
3	5	0.009999997	3.476320572	0.000508344
3	6	0.009999997	3.526908572	0.000420442
4	5	0.009999942	3.06127534	0.002203963
4	6	0.009999996	3.220568965	0.001279364
5	6	0.009999971	3.330876037	0.000865731

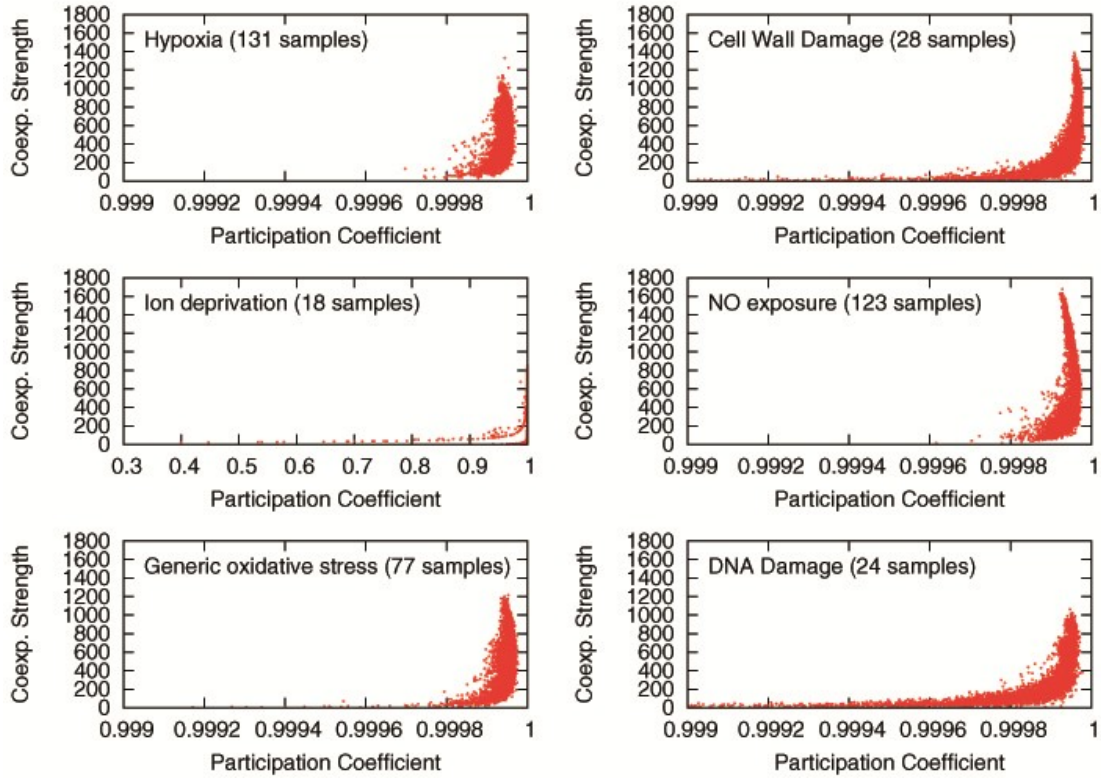
Appendix D. Other graphics of gene-coexpression analysis.

D.1. Strength vs degree



On x-axis, degree (number of connections of a given node). On y axis, coexpression strength, sum of the strengths of all interactions of a given node. Each spot on the graphs represents a given gene. This almost linear trend in most of the conditions shows that the strength of a gene is almost directly proportional to the number of links it has, so all interactions should be of a similar strength. However, not much more information about the system studied in this work can be extracted from these graphs.

D.2. Strength vs participation coefficient



On x-axis, participation coefficient (see equation (10) on the main text). On y axis, coexpression strength, sum of the strengths of all interactions of a given node. Each spot on the graphs represents a given gene. Except for ion deprivation, the scale in all of the cases for participation coefficient goes from 0.999 to 1, which is a really small change. This means that almost all interactions are the same, reinforcing the idea taken from the graphs in appendix D.1. Probably all of this is a consequence of generating very dense networks, and that would explain also why this is not happening on ion deprivation. However, most of the data in that case is also between 0.9 and 1, showing probably that this network has some genes where not all interactions are nearly the same strength.

Appendix E. Full DAVID enrichment analysis results.

All results obtained from data enrichment in DAVID are showed here, with the number of genes belonging to each overexpressed category, the p-value showing the probability of having that overrepresentation in a randomly selected set of genes, and the fold enrichment (F. E.). This enrichment has been performed with Gene Ontology terms (GO terms) for biological processes and with terms from KEGG Pathway database. Both of them are shown in the following appendix. In all cases, enrichment is performed for the 100 genes with higher strength for each condition, unless otherwise stated. Default parameters for DAVID gene enrichment are used, where thresholds considered for significant terms is p-value under 0.1 and gene count of at least 2.

E.1. Enrichment in layer 0, hypoxia

A. GO terms

Term	Count	%	P-Value	F. E.
photosynthesis, light reaction	4	4.4	9.70E-06	77.6
photosynthesis	4	4.4	7.90E-05	43.1
generation of precursor metabolites and energy	8	8.8	5.60E-04	5.4
plasma membrane ATP synthesis coupled proton transport	3	3.3	9.90E-04	58.2
hydrogen transport	4	4.4	1.10E-03	18.5
ATP synthesis coupled proton transport	4	4.4	1.10E-03	18.5
proton transport	4	4.4	1.10E-03	18.5
energy coupled proton transport, down electrochemical gradient	4	4.4	1.10E-03	18.5
ion transmembrane transport	4	4.4	2.70E-03	13.9
oxidative phosphorylation	4	4.4	7.50E-03	9.7
monovalent inorganic cation transport	4	4.4	1.00E-02	8.6
transmembrane transport	4	4.4	1.40E-02	7.8
ATP biosynthetic process	4	4.4	2.00E-02	6.8
ATP metabolic process	4	4.4	2.00E-02	6.8
purine ribonucleoside triphosphate biosynthetic process	4	4.4	2.00E-02	6.7
ribonucleoside triphosphate biosynthetic process	4	4.4	2.00E-02	6.7
purine nucleoside triphosphate biosynthetic process	4	4.4	2.00E-02	6.7
ribonucleoside triphosphate metabolic process	4	4.4	2.30E-02	6.4
purine nucleoside triphosphate metabolic process	4	4.4	2.30E-02	6.4
purine ribonucleoside triphosphate metabolic process	4	4.4	2.30E-02	6.4
nucleoside triphosphate biosynthetic process	4	4.4	2.30E-02	6.4
nucleoside triphosphate metabolic process	4	4.4	2.80E-02	6
cellular amino acid derivative biosynthetic process	3	3.3	3.20E-02	10.4
purine ribonucleotide biosynthetic process	4	4.4	4.50E-02	4.9
purine ribonucleotide metabolic process	4	4.4	5.00E-02	4.7
ribonucleotide biosynthetic process	4	4.4	5.30E-02	4.6
ribonucleotide metabolic process	4	4.4	5.70E-02	4.5
establishment of localization	11	12.1	5.90E-02	1.9
transport	11	12.1	5.90E-02	1.9

localization	11	12.1	6.10E-02	1.9
purine nucleotide biosynthetic process	4	4.4	6.70E-02	4.2
cellular amino acid derivative metabolic process	3	3.3	7.30E-02	6.6
purine nucleotide metabolic process	4	4.4	7.40E-02	4
ion transport	6	6.6	8.50E-02	2.5
indole and derivative metabolic process	2	2.2	8.80E-02	21.6
tryptophan biosynthetic process	2	2.2	8.80E-02	21.6
tryptophan metabolic process	2	2.2	8.80E-02	21.6
indolalkylamine metabolic process	2	2.2	8.80E-02	21.6
indole derivative metabolic process	2	2.2	8.80E-02	21.6
indolalkylamine biosynthetic process	2	2.2	8.80E-02	21.6
indole derivative biosynthetic process	2	2.2	8.80E-02	21.6
cellular metabolic process	33	36.3	9.60E-02	1.2

B. KEGG

Term	Count	%	P-Value	F. E.
Oxidative phosphorylation	7	7.7	4.30E-05	9.9
Oxidative phosphorylation	7	7.7	4.90E-05	9.7
Oxidative phosphorylation	7	7.7	4.90E-05	9.7
Selenoamino acid metabolism	6	6.6	1.90E-04	10.3
Histidine metabolism	4	4.4	2.10E-02	6.5
Tyrosine metabolism	4	4.4	2.20E-02	6.4
Pantothenate and CoA biosynthesis	3	3.3	3.00E-02	10.6
Pantothenate and CoA biosynthesis	3	3.3	3.00E-02	10.6
Cysteine and methionine metabolism	3	3.3	4.30E-02	8.7
Cysteine and methionine metabolism	3	3.3	4.30E-02	8.7
Androgen and estrogen metabolism	3	3.3	6.70E-02	6.8
Polyketide sugar unit biosynthesis	2	2.2	7.40E-02	25.4
Polyketide sugar unit biosynthesis	2	2.2	8.80E-02	21.2
Selenoamino acid metabolism	3	3.3	8.90E-02	5.8

E.2. Enrichment in layer 2, cell wall damage

A. GO terms

Term	Count	%	P-Value	F.E.
cellular biosynthetic process	24	26.7	7.20E-04	1.9
biosynthetic process	26	28.9	8.30E-04	1.8
cellular macromolecule biosynthetic process	14	15.6	5.50E-03	2.2
macromolecule biosynthetic process	14	15.6	6.40E-03	2.2
gene expression	12	13.3	1.80E-02	2.1
primary metabolic process	29	32.2	4.00E-02	1.3
plasma membrane ATP synthesis coupled proton transport	2	2.2	4.10E-02	47.1

response to antibiotic	3	3.3	6.00E-02	7.4
transmembrane transport	3	3.3	6.40E-02	7.1
translation	4	4.4	7.30E-02	4
response to chemical stimulus	3	3.3	7.90E-02	6.3
protein metabolic process	8	8.9	9.30E-02	2
macromolecule metabolic process	19	21.1	9.70E-02	1.4
response to stimulus	6	6.7	9.80E-02	2.4
nucleobase, nucleoside and nucleotide biosynthetic process	5	5.6	9.90E-02	2.8
nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	5	5.6	9.90E-02	2.8

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	3	3.3	6.20E-02	6.9
Ribosome	3	3.3	6.40E-02	6.7
Ribosome	3	3.3	6.70E-02	6.6
Purine metabolism	3	3.3	7.70E-02	6.1
Purine metabolism	3	3.3	7.70E-02	6.1
Purine metabolism	3	3.3	8.00E-02	6

E.3. Enrichment in layer 3, ion deprivation

A. GO terms

Term	Count	%	P-Value	F. E.
translation	14	16.1	9.00E-12	13.5
cellular protein metabolic process	14	16.1	5.40E-07	5.5
gene expression	19	21.8	4.90E-06	3.2
macromolecule biosynthetic process	20	23	6.20E-06	3
cellular macromolecule biosynthetic process	19	21.8	2.00E-05	2.9
protein metabolic process	15	17.2	2.90E-05	3.6
macromolecule metabolic process	24	27.6	4.70E-03	1.7
cellular macromolecule metabolic process	21	24.1	9.10E-03	1.7
biosynthetic process	24	27.6	1.00E-02	1.6
cellular biosynthetic process	21	24.1	1.90E-02	1.6
primary metabolic process	30	34.5	4.20E-02	1.3
cellular metabolic process	30	34.5	5.00E-02	1.3
metabolic process	46	52.9	5.10E-02	1.1
cellular process	31	35.6	9.00E-02	1.2

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	13	14.9	2.80E-12	15.7
Ribosome	13	14.9	3.60E-12	15.5
Ribosome	13	14.9	4.50E-12	15.2
Ribosome	12	13.8	7.80E-11	14.5

E.4. Enrichment in layer 4, NO exposure

A. GO terms

Term	Count	%	P-Value	F. E.
translation	19	21.1	4.30E-18	16.9
cellular protein metabolic process	24	26.7	9.30E-17	8.8
protein metabolic process	24	26.7	5.30E-12	5.3
cellular macromolecule biosynthetic process	22	24.4	9.90E-07	3.1
biosynthetic process	34	37.8	1.30E-06	2.1
macromolecule biosynthetic process	22	24.4	1.40E-06	3.1
gene expression	20	22.2	4.20E-06	3.1
primary metabolic process	41	45.6	9.30E-06	1.6
cellular macromolecule metabolic process	27	30	9.90E-05	2
cellular biosynthetic process	27	30	3.30E-04	1.9
macromolecule metabolic process	27	30	1.30E-03	1.7
cellular metabolic process	35	38.9	7.10E-03	1.4
cellular process	37	41.1	8.00E-03	1.3
protein folding	3	3.3	1.60E-02	14.9
aromatic amino acid family metabolic process	3	3.3	3.80E-02	9.5
chorismate metabolic process	3	3.3	3.80E-02	9.5
aromatic amino acid family biosynthetic process	3	3.3	3.80E-02	9.5
lipid metabolic process	7	7.8	4.70E-02	2.6
lipid biosynthetic process	5	5.6	5.70E-02	3.4
indole derivative biosynthetic process	2	2.2	8.20E-02	23.2
tryptophan biosynthetic process	2	2.2	8.20E-02	23.2
indole and derivative metabolic process	2	2.2	8.20E-02	23.2
tryptophan metabolic process	2	2.2	8.20E-02	23.2
indolalkylamine metabolic process	2	2.2	8.20E-02	23.2
indole derivative metabolic process	2	2.2	8.20E-02	23.2
indolalkylamine biosynthetic process	2	2.2	8.20E-02	23.2
metabolic process	49	54.4	8.40E-02	1.1

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	16	17.8	9.80E-17	18.8
Ribosome	16	17.8	9.80E-17	18.8
Ribosome	16	17.8	1.30E-16	18.5
Ribosome	16	17.8	1.80E-16	18.1
Phenylalanine, tyrosine and tryptophan biosynthesis	3	3.3	3.00E-02	10.6

E.5. Enrichment in layer 5, generic oxidative stress

A. GO terms

Term	Count	%	P-Value	F. E.
translation	8	8.7	1.10E-04	7
cell cycle	6	6.5	4.10E-04	9.2
cellular protein metabolic process	10	10.9	1.40E-03	3.6
protein metabolic process	12	13	4.40E-03	2.6
cell division	5	5.4	4.80E-03	7.1
cellular macromolecule biosynthetic process	15	16.3	7.70E-03	2.1
macromolecule biosynthetic process	15	16.3	9.10E-03	2.1
sulfate assimilation	2	2.2	4.70E-02	41
cellular process	35	38	4.70E-02	1.3
gene expression	12	13	4.80E-02	1.8
cellular macromolecule metabolic process	19	20.7	9.80E-02	1.4

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	7	7.6	1.50E-05	11.5
Ribosome	7	7.6	1.50E-05	11.5
Ribosome	7	7.6	1.70E-05	11.3
Ribosome	7	7.6	1.80E-05	11.1
Oxidative phosphorylation	5	5.4	1.20E-03	9.9
Oxidative phosphorylation	5	5.4	1.30E-03	9.7
Oxidative phosphorylation	5	5.4	1.30E-03	9.7
Sulfur metabolism	2	2.2	9.30E-02	19.8

E.6. Enrichment in layer 6, DNA damage

A. GO terms

Term	Count	%	P-Value	F. E.
heterocycle metabolic process	7	8	2.60E-02	2.9
cellular biosynthetic process	15	17	8.10E-02	1.5
purine ribonucleotide biosynthetic process	3	3.4	9.30E-02	5.7
purine ribonucleotide metabolic process	3	3.4	9.90E-02	5.5

B. KEGG

Term	Count	%	P-Value	F. E.
Two-component system	5	5.7	1.70E-03	8.9
Pyruvate metabolism	4	4.5	6.20E-03	9.9
Benzoate degradation via CoA ligation	4	4.5	2.60E-02	5.9
Pyruvate metabolism	3	3.4	5.60E-02	7.4
Oxidative phosphorylation	3	3.4	6.60E-02	6.7
Oxidative phosphorylation	3	3.4	6.90E-02	6.6
Oxidative phosphorylation	3	3.4	6.90E-02	6.6
Naphthalene and anthracene degradation	3	3.4	8.50E-02	5.8
Two-component system	3	3.4	9.90E-02	5.3

E.7. Enrichment in overlap

A. GO terms

Term	Count	%	P-Value	F. E.
translation	14	15.2	7.60E-11	11.6
cellular protein metabolic process	17	18.5	1.10E-08	5.8
protein metabolic process	19	20.7	4.20E-07	3.9
gene expression	19	20.7	5.60E-05	2.8
cellular macromolecule biosynthetic process	20	21.7	6.00E-05	2.6
macromolecule biosynthetic process	20	21.7	7.80E-05	2.6
biosynthetic process	31	33.7	3.60E-04	1.8
photosynthesis, light reaction	3	3.3	9.90E-04	58.2
cellular biosynthetic process	27	29.3	1.40E-03	1.8
photosynthesis	3	3.3	3.50E-03	32.3
cellular process	40	43.5	5.00E-03	1.4
localization	13	14.1	1.10E-02	2.2
cellular macromolecule metabolic process	23	25	1.40E-02	1.6
generation of precursor metabolites and energy	6	6.5	1.50E-02	4
cellular metabolic process	36	39.1	1.70E-02	1.3
transport	12	13	2.60E-02	2
establishment of localization	12	13	2.60E-02	2
macromolecule metabolic process	24	26.1	3.90E-02	1.4
protein localization	3	3.3	3.90E-02	9.4
macromolecule localization	3	3.3	4.40E-02	8.8
oxidative phosphorylation	3	3.3	6.10E-02	7.3
indolalkylamine biosynthetic process	2	2.2	8.80E-02	21.6
indole derivative biosynthetic process	2	2.2	8.80E-02	21.6
tryptophan metabolic process	2	2.2	8.80E-02	21.6
indolalkylamine metabolic process	2	2.2	8.80E-02	21.6
tryptophan biosynthetic process	2	2.2	8.80E-02	21.6
indole derivative metabolic process	2	2.2	8.80E-02	21.6
indole and derivative metabolic process	2	2.2	8.80E-02	21.6
transmembrane transport	3	3.3	9.10E-02	5.8

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	13	14.1	6.40E-12	14.9
Ribosome	13	14.1	8.20E-12	14.6
Ribosome	13	14.1	1.00E-11	14.3
Ribosome	12	13	1.60E-10	13.7
Oxidative phosphorylation	8	8.7	3.80E-06	11
Oxidative phosphorylation	8	8.7	4.40E-06	10.7
Oxidative phosphorylation	8	8.7	4.40E-06	10.7

E.8. Enrichment in all genes with multiplex participation coefficient under 0.8

A. GO terms

Term	Count	%	P-Value	F. E.
cellular macromolecule biosynthetic process	29	10.6	3.60E-03	1.7
cellular biosynthetic process	49	17.9	4.00E-03	1.4
macromolecule biosynthetic process	29	10.6	4.80E-03	1.7
biosynthetic process	53	19.4	9.10E-03	1.3
metabolic process	117	42.9	9.90E-03	1.1
gene expression	25	9.2	1.40E-02	1.6
primary metabolic process	72	26.4	2.10E-02	1.2
nitrogen compound metabolic process	55	20.1	2.20E-02	1.3
nucleoside monophosphate biosynthetic process	7	2.6	2.30E-02	3.1
nucleoside monophosphate metabolic process	7	2.6	2.30E-02	3.1
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	43	15.8	2.30E-02	1.3
cellular macromolecule metabolic process	43	15.8	2.40E-02	1.3
transcription	18	6.6	3.60E-02	1.7
cellular nitrogen compound metabolic process	51	18.7	5.00E-02	1.2
intracellular signaling cascade	5	1.8	6.30E-02	3.3
oxidation reduction	30	11	6.50E-02	1.4
macromolecule metabolic process	46	16.8	6.80E-02	1.2
cyclic nucleotide biosynthetic process	5	1.8	6.90E-02	3.2
cyclic nucleotide metabolic process	5	1.8	6.90E-02	3.2
DNA integration	6	2.2	8.20E-02	2.6
cellular metabolic process	69	25.3	8.70E-02	1.1

B. KEGG

Term	Count	%	P-Value	F. E.
Limonene and pinene degradation	9	3.3	8.50E-04	4.3
Naphthalene and anthracene degradation	7	2.6	3.50E-03	4.5
Nucleotide excision repair	4	1.5	6.90E-03	9.6
Nucleotide excision repair	4	1.5	6.90E-03	9.6
Nucleotide excision repair	4	1.5	6.90E-03	9.6
Benzoate degradation via CoA ligation	7	2.6	1.40E-02	3.4
Geraniol degradation	6	2.2	2.70E-02	3.4
Valine, leucine and isoleucine degradation	6	2.2	2.90E-02	3.4
Limonene and pinene degradation	6	2.2	3.90E-02	3.1
Glycerophospholipid metabolism	4	1.5	4.20E-02	5
Butanoate metabolism	6	2.2	4.60E-02	3
Lysine degradation	5	1.8	4.60E-02	3.6
Tryptophan metabolism	5	1.8	4.90E-02	3.5
gamma-Hexachlorocyclohexane degradation	4	1.5	6.00E-02	4.3
Caprolactam degradation	4	1.5	6.00E-02	4.3
Fatty acid metabolism	5	1.8	6.30E-02	3.2

E.9. Enrichment in all genes with positive cosine similarity index for one or more layers

A. GO terms

Term	Count	%	P-Value	F. E.
translation	40	7.4	2.40E-22	6.6
cellular protein metabolic process	48	8.9	3.70E-13	3.2
biosynthetic process	144	26.8	5.50E-12	1.6
protein metabolic process	58	10.8	4.30E-10	2.4
cellular biosynthetic process	123	22.9	3.40E-09	1.6
macromolecule biosynthetic process	71	13.2	2.30E-07	1.8
cellular macromolecule biosynthetic process	70	13	2.40E-07	1.8
gene expression	65	12.1	3.20E-07	1.9
ribonucleoside monophosphate biosynthetic process	9	1.7	1.20E-05	7.5
ribonucleoside monophosphate metabolic process	9	1.7	1.20E-05	7.5
purine nucleoside monophosphate metabolic process	8	1.5	2.70E-05	8.1
purine ribonucleoside monophosphate biosynthetic process	8	1.5	2.70E-05	8.1
purine nucleoside monophosphate biosynthetic process	8	1.5	2.70E-05	8.1
purine ribonucleoside monophosphate metabolic process	8	1.5	2.70E-05	8.1
primary metabolic process	168	31.3	4.60E-05	1.2
cellular metabolic process	167	31.1	1.70E-04	1.2
cellular process	178	33.1	2.80E-04	1.2
IMP biosynthetic process	6	1.1	3.30E-04	8.9

IMP metabolic process	6	1.1	3.30E-04	8.9
ribonucleotide metabolic process	14	2.6	4.70E-04	3.1
purine ribonucleotide metabolic process	13	2.4	9.30E-04	3.1
ribonucleotide biosynthetic process	13	2.4	1.20E-03	3
purine ribonucleotide biosynthetic process	12	2.2	2.30E-03	2.9
'de novo' IMP biosynthetic process	5	0.9	2.50E-03	8
metabolic process	259	48.2	3.60E-03	1.1
purine nucleotide metabolic process	13	2.4	4.00E-03	2.6
cellular macromolecule metabolic process	93	17.3	4.10E-03	1.3
cellular component organization	13	2.4	7.60E-03	2.4
purine nucleotide biosynthetic process	12	2.2	8.10E-03	2.5
indole and derivative metabolic process	4	0.7	9.10E-03	8.6
tryptophan metabolic process	4	0.7	9.10E-03	8.6
indolalkylamine metabolic process	4	0.7	9.10E-03	8.6
indolalkylamine biosynthetic process	4	0.7	9.10E-03	8.6
tryptophan biosynthetic process	4	0.7	9.10E-03	8.6
indole derivative biosynthetic process	4	0.7	9.10E-03	8.6
indole derivative metabolic process	4	0.7	9.10E-03	8.6
macromolecule metabolic process	103	19.2	9.70E-03	1.2
response to antibiotic	8	1.5	1.10E-02	3.2
nucleoside monophosphate metabolic process	12	2.2	1.10E-02	2.4
nucleoside monophosphate biosynthetic process	12	2.2	1.10E-02	2.4
lipid biosynthetic process	16	3	1.40E-02	2
heterocycle metabolic process	29	5.4	1.70E-02	1.6
photosynthesis, light reaction	3	0.6	2.40E-02	11.6
response to chemical stimulus	8	1.5	2.40E-02	2.8
chorismate metabolic process	6	1.1	2.60E-02	3.5
aromatic amino acid family biosynthetic process	6	1.1	2.60E-02	3.5
aromatic amino acid family metabolic process	6	1.1	2.60E-02	3.5
biogenic amine biosynthetic process	4	0.7	3.30E-02	5.5
nitrogen compound biosynthetic process	39	7.3	3.80E-02	1.4
organic acid metabolic process	31	5.8	3.80E-02	1.4
amine metabolic process	27	5	4.10E-02	1.5
cytokinesis	3	0.6	4.70E-02	8.3
barrier septum formation	3	0.6	4.70E-02	8.3
cytokinetic process	3	0.6	4.70E-02	8.3
nucleobase, nucleoside and nucleotide biosynthetic process	18	3.4	4.80E-02	1.6
nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	18	3.4	4.80E-02	1.6
cellular amino acid metabolic process	22	4.1	5.00E-02	1.5
carboxylic acid metabolic process	30	5.6	5.10E-02	1.4
oxoacid metabolic process	30	5.6	5.10E-02	1.4
nucleotide biosynthetic process	17	3.2	5.30E-02	1.6

cellular component biogenesis	12	2.2	6.00E-02	1.8
cellular ketone metabolic process	30	5.6	6.30E-02	1.4
external encapsulating structure organization	5	0.9	7.30E-02	3.1
cell wall organization	5	0.9	7.30E-02	3.1
photosynthesis	3	0.6	7.50E-02	6.4
phospholipid biosynthetic process	5	0.9	8.10E-02	3
cellular amine metabolic process	22	4.1	8.80E-02	1.4
lipid metabolic process	21	3.9	8.80E-02	1.4
dicarboxylic acid metabolic process	7	1.3	9.40E-02	2.2
carbohydrate biosynthetic process	9	1.7	9.70E-02	1.9

B. KEGG

Term	Count	%	P-Value	F. E.
Ribosome	31	5.8	1.80E-22	8.4
Ribosome	31	5.8	3.80E-22	8.2
Ribosome	30	5.6	1.40E-20	7.8
Ribosome	29	5.4	6.80E-20	7.9
Purine metabolism	18	3.4	2.30E-07	4.3
Purine metabolism	18	3.4	3.00E-07	4.2
Purine metabolism	16	3	7.00E-06	3.8
Phenylalanine, tyrosine and tryptophan biosynthesis	6	1.1	5.60E-03	4.9
Taurine and hypotaurine metabolism	4	0.7	8.80E-03	8.4
Propanoate metabolism	11	2	1.20E-02	2.4
Pyruvate metabolism	8	1.5	1.80E-02	2.9
Pyruvate metabolism	8	1.5	1.80E-02	2.9
Biosynthesis of siderophore group nonribosomal peptides	4	0.7	1.90E-02	6.5
Biosynthesis of siderophore group nonribosomal peptides	4	0.7	1.90E-02	6.5
Atrazine degradation	3	0.6	2.50E-02	11
Oxidative phosphorylation	8	1.5	3.00E-02	2.6
Phenylalanine, tyrosine and tryptophan biosynthesis	5	0.9	3.00E-02	4.1
Propanoate metabolism	10	1.9	3.20E-02	2.2
Oxidative phosphorylation	8	1.5	3.30E-02	2.5
Oxidative phosphorylation	8	1.5	3.30E-02	2.5
Phenylalanine, tyrosine and tryptophan biosynthesis	5	0.9	3.60E-02	3.8
Selenoamino acid metabolism	7	1.3	3.60E-02	2.8
Two-component system	9	1.7	3.60E-02	2.3
Two-component system	9	1.7	3.60E-02	2.3
One carbon pool by folate	4	0.7	4.30E-02	4.9
One carbon pool by folate	4	0.7	4.30E-02	4.9
One carbon pool by folate	4	0.7	4.30E-02	4.9
Taurine and hypotaurine metabolism	3	0.6	7.70E-02	6.3
ABC transporters	8	1.5	8.80E-02	2.1

Appendix F. Genes with positive cosine similarity index

Here, the genes with positive cosine similarity index for one or more differential coexpression layers are shown, showing in which layers they get a positive value. In the top line, differential layers, showing the layers being compared as expressed in figure 7. Below, the total number of positive for each line is shown. Then, positives for each gene are represented, being 1 a positive value and 0 a negative one. On the right column, total of positive interactions, being green the higher number of positives and red the lower. Results are shown in decreasing number of interactions.

Layers	0→2	0→3	0→4	0→5	0→6	2→3	2→4	2→5	2→6	3→4	3→5	3→6	4→5	4→6	5→6	TOTAL
TOTAL	115	31	102	36	0	9	53	89	0	36	30	9	286	0	18	814
Rv0396	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	4
Rv0957	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	4
Rv1201c	1	0	1	0	0	0	0	1	0	0	0	0	1	0	0	4
Rv1770	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	4
Rv3553	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	4
Rv2973c	0	1	0	0	0	0	0	1	0	1	1	0	0	0	0	4
Rv0642c	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	4
Rv0635	0	1	1	1	0	0	0	0	0	0	0	0	1	0	0	4
Rv3671c	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	3
Rv1980c	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv0177	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv3040c	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	3
Rv0563	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	3
Rv1613	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv0733	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	3
Rv1919c	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	3
Rv3742c	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	3
Rv3752c	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	3
Rv1671	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	3
Rv2954c	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	3
Rv3061c	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	3
Rv1528c	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv2929	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv1806	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	3
Rv0701	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv0700	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	3
Rv2882c	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	3
Rv0315	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	3
Rv3503c	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv2312	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv3624c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv3392c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1584c	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv0935	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0412c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2

Rv0203	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv0316	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv2728c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2272	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1977	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3647c	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv0430	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2872	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv0251c	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv1674c	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
Rv1643	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1641	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv3148	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1230c	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv0178	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0176	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0003	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0001	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2324	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
Rv1569	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
Rv0164	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0167	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3276c	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv0185	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv2082	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1285	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3281	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2228c	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv0773c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3920c	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
Rv1610	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
Rv1612	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0961	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2
Rv0967	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv1168c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv3725	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0637	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0636	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2526	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv0702	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2395	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
Rv2067c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0732	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3181c	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv0566c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3629c	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2

Rv2062c	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv3854c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1711	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1710	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2
Rv1713	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2
Rv2048c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv0140	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	2
Rv1990c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv3504	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv2389c	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2
Rv2359	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv2083	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv1431	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
Rv2018	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv0654	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv0867c	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv2881c	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv2445c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv3545c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv0220	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
Rv0780	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
Rv1311	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv0595c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv1222	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1016c	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	2
Rv2192c	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
Rv3000	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
Rv1421	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv0009	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv3078	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1101c	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv1885c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv2701c	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	2
Rv0761c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv2711	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv3411c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv0760c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv0721	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv0956	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1073	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv0830	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv3060c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv2582	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1219c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv0460	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv1805c	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2

Rv2128	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1577c	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv2826c	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0022c	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2
Rv2442c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3924c	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv2928	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0010c	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
Rv0677c	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv3589	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv1605	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Rv3577	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0067c	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv2617c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv1673c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
Rv2279	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2
Rv1649	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2357c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3330	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0165c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0198c	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3065	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv1894c	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv2957	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2465c	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0360c	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Rv3713	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv0446c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv1992c	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1050	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv1118c	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
Rv0244c	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv0584	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
Rv0197	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv0402c	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv3807c	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv3556c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
Rv3029c	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv2956	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2744c	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0640	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv2707	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Rv0237	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
Rv3726	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv0236c	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
Rv2201	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2

Rv1839c	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Rv0684	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
Rv3534c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2949c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3833	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0549c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3334	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3890c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2798c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2053c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1689	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1158c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1664	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0934	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0933	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2955c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1338	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv0682	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0685	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1241	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1240	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0331	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3891c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv0750	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0605	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3922c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Rv2453c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2382c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1697	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1622c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3747	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3871	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2271	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1464	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0705	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1310	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3770c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv1433	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0694	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Rv0925c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1467c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3458c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3478	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0273c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1989c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0704	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1

Rv3869	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Rv0643c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv3378c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0774c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Rv0669c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv1993c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv3125c	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Rv3459c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0077c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv3527	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv3579c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2822c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Rv0006	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0007	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2994	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv0953c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Rv1133c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Rv2346c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Rv0116c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2947c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv3703c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Rv2216	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv0644c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2506	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Rv3496c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Rv0340	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0950c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv1897c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Rv0874c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0276	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv2169c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0170	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0039c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv2381c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2124c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Rv1623c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2710	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv3515c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv0712	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv2462c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv2888c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv3678c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv3402c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rv0936	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rv2527	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Rv1614	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Rv1611	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2684	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2156c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1769	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv1546	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1704c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2372c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0722	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2390c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2383c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3136	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0059	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2147c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0883c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3921c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0954	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0952	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2463	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2151c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2011c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1152	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0554	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0758	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3206c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3146	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3147	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1808	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2520c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1708	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1677	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0723	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0057	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3290c	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0222	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1576c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1478	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2967c	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Rv1479	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3150	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2150c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1955	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0847	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1003	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0915c	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Rv0668	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2640c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Rv0846c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3574	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0429c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0786c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv0824c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3734c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2102	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2288	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0072	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2330c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0188	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3753c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2946c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv1025	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0514	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv0510	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0409	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv2908c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3292	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv2468c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3224	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3335c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3487c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2017	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2016	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2012	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2905	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3692	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3526	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3570c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2197c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3858c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1586c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv2902c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1461	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0190	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3161c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3537	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3538	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2015c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2745c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3277	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0132c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3571	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv1639c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv0225	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1

Rv2001	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1559	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv1015c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2909c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1095	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv0418	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2674	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2679	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv0300	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3331	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3797	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3872	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1509	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv2651c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0211	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1445c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0444c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Rv1646	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0168	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3066	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2220	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3669	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1571	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0158	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3268	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv1147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv2652c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3546	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2516c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1836c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0472c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv2277c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2450c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2616	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2152c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1218c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv1484	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3460c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0280	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
Rv2971	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0902c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv1822	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2740	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3766	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv0451c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1397c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1

Rv1849	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv1848	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2633c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2123	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0248c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1846c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3748	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3744	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv3524	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3923c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1875	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3885c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2754c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3754	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
Rv2412	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1465	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2930	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv0134	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv0788	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1111c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv1098c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1672c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2536	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3275c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2441c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1075c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0909	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3846	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0447c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0707	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3140	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2688c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2289	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3101c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2778c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0734	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3836	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2430c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2190c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2134c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2729c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3794	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0484c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv1345	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3476c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0411c	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1

Rv3311	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1991c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3808c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2227	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1192	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0379	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0716	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0715	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3285	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv3139	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2953	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3899c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv0275c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1720c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2650c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv1474c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv0678	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv0573c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv3396c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv0462	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3032	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv2620c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1507c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1876	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2339	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2981c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1466	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1463	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1845c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0557	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv0108c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3403c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2344c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv0891c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3914	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0586	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2980	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv3843c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2140c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0622	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv2348c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv2952	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3580c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1026	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0755c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv0408	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Rv2673	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0714	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0717	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1462	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1116	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Rv0227c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3795	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv2276	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3068c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Rv1515c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0718	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0710	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1350	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv1360	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2890c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0485	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv0809	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv2380c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3424c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv0355c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0703	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1460	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0829	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2364c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv1492	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1011	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0617	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv1721c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3404c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3442c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0196	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2522c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0245	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2612c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3909	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2965c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1428c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2968c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2502c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3342	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv0596c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3839	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3002c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0894	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv2903c	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2632c	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1

Rv1096	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1901	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3288c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1982c	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0021c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2275	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1017c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3456c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0741	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1358	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Rv0171	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2660c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv1286	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0719	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1252c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2998	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3406	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv0213c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Rv3613c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv2951c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv2499c	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Rv3722c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0827c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3614c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv0879c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv3715c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3087	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2329c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3463	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3180c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3398c	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3188	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0425c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2459	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv2797c	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Rv3586	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3793	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1132	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1244	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0060	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2495c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0068	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3054c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0476	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3664c	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Rv0307c	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1

Rv1941	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3438	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv0988	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3160c	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv2849c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Rv3134c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Rv3089	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1078	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv1607	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv0667	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv3297	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1502	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Rv0949	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv1189	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3435c	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Rv3904c	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1

Appendix G. Detailed information about the genes with positive cosine similarity index in 3 or 4 layers

Here, the list of genes with positive cosine similarity index is given. First column is its Rv number, second shows the differential layers in which they have positive cosine similarity index. The third column shows the protein they are encoding and the last shows its function.

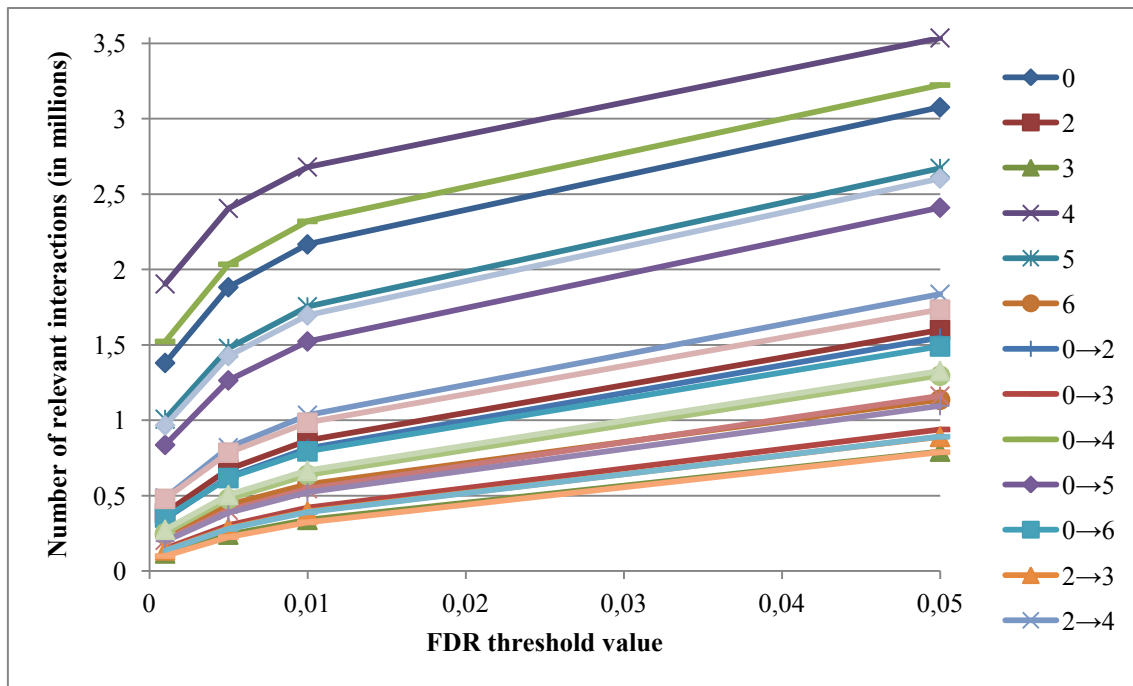
Rv number	Positive in	Coding for [†]	Function [†]
Rv0177	0→2 0→4 4→5	Probable conserved Mce (mammalian cell entry) associated protein	Unknown, probably related to virulence
Rv0315	0→2 0→4 0→5	Possible beta-1,3-glucanase precursor	Possibly hydrolyzes specific sugar. Possible biosynthesis/degradation of exopolysaccharide. Possible lytic activity against cell walls
Rv0396	2→3 3→4 3→5 3→6	Hypothetical protein	Unknown
Rv0563	0→2 2→4 4→5	Probable protease transmembrane protein heat shock protein HtpX	Possibly involved in adaptation. Hydrolyzes specific peptides and/or proteins
Rv0635	0→3 0→4 0→5 4→5	(3R)-hydroxyacyl-ACP dehydratase subunit HadA	Involved in fatty acid synthesis type II (fas-II)
Rv0642c	0→2 0→4 0→5 4→5	Methoxy mycolic acid synthase 4 MmaA4	Involved in mycolic acids modification, major constituents of the cell wall
Rv0700	0→4 0→5 4→5	30S ribosomal protein S10 RpsJ	Binding of tRNA to the ribosomes and regulation of rRNA biosynthesis
Rv0701	0→4 0→5 4→5	50S ribosomal protein L3 RplC	Binds to 23S ribosomal RNA and may participate in the peptidyltransferase center of the ribosome
Rv0733	0→4 2→5 4→5	Adenylate kinase Adk	Intracellular nucleotide metabolism, possible role in RNA and DNA synthesis
Rv0957	0→2 0→3 0→4 4→5	Probable bifunctional purine biosynthesis protein PurH	De novo purine biosynthesis, intermediary metabolism and respiration
Rv1201c	0→2 0→4 2→5 4→5	Tetrahydrodipicolinate N-succinyltransferase DapD	Biosynthesis of diaminopimelate and lysine from aspartate semialdehyde
Rv1528c	0→2 0→5 4→5	Probable conserved polyketide synthase associated protein PapA4	Unknown; thought to be involved in lipid metabolism
Rv1613	0→4 0→5 4→5	Probable tryptophan synthase, alpha subunit TrpA	Tryptophan biosynthesis pathway
Rv1671	0→2 2→4 2→5	Probable membrane protein	Unknown
Rv1770	0→2 0→4 0→5 4→5	Conserved protein	Unknown
Rv1806	0→2 2→4 2→5	PE family protein PE20	Unknown; possible MT-complex-specific genomic island
Rv1919c	0→2 0→4 4→5	Conserved protein	Unknown
Rv1980c	0→4 0→5 4→5	Immunogenic protein Mpt64 (antigen Mpt64/MPB64)	Unknown, probably involved in cell wall processes
Rv2882c	0→2 0→4 4→5	Ribosome recycling factor Frr	Release of ribosomes from mRNA at the termination of protein biosynthesis
Rv2929	0→4 0→5 4→5	Hypothetical protein	Unknown; possible MT-complex-specific genomic island
Rv2954c	0→4 2→5 4→5	Hypothetical protein	Unknown; possible MT-complex-specific genomic island
Rv2973c	0→3 2→5 3→4 3→5	Probable ATP-dependent DNA helicase RecG	Recombination and DNA repair
Rv3040c	0→2 2→4 2→5	Conserved protein	Unknown
Rv3061c	3→4 3→5 3→6	Probable acyl-CoA dehydrogenase FadE22	Unknown, but involved in lipid degradation
Rv3553	2→3 3→4 3→5 3→6	Possible oxidoreductase	Probably involved in cellular intermediary metabolism and respiration
Rv3671c	0→2 0→4 4→5	Membrane-associated serine protease	Unknown; hydrolyses of peptides and/or proteins (possibly cleaved preferentially after serine residue)
Rv3742c	0→2 2→4 2→5	Possible oxidoreductase	Unknown; probably involved in cellular metabolism.
Rv3752c	2→3 3→4 3→5	Possible cytidine/deoxycytidylate deaminase	Unknown; probably involved in deamination of specific substrate

[†] Data obtained from TubercuList [26]

Appendix H. Thresholding effect on positive interactions.

In this appendix, the number of statistically significant interactions depending on the value chosen for the FDR threshold is shown. The values chosen for thresholding here are the most commonly used.

Layer	0.05	0.01	0.005	0.001
0	3076123	2167154	1882992	1380917
2	1599116	866719	675079	386657
3	793086	340609	242707	117818
4	3536008	2680360	2405586	1904855
5	2671384	1754234	1478282	1008338
6	1137064	575057	439082	243911
0→2	1548056	813183	625119	347593
0→3	939818	420806	304972	149518
0→4	3223491	2319820	2035050	1523379
0→5	2410707	1523681	1265317	837399
0→6	1490186	794534	617543	354665
2→3	890686	395866	285041	138469
2→4	1836822	1034664	819353	487084
2→5	1161810	547147	403266	204339
2→6	1296641	638228	479165	252344
3→4	1096552	522154	386236	198984
3→5	891751	391270	280906	135276
3→6	789084	323612	225520	100747
4→5	2604050	1696384	1426189	967115
4→6	1734503	984721	786166	479523
5→6	1327916	666349	505748	274895



In this figure, the values showed in the table are graphically represented. On the right, the legend showing which line corresponds to which layer is shown. On x-axis, FDR threshold values are shown and, in y-axis, the number in millions of interactions that are considered statistically significant with that threshold.

Appendix I. Simulation of the statistical method

As our method for calculating p-values for Spearman coefficients was only described for samples with a size equal to 50 or lower, a statistical simulation of the method was necessary to check this approximation is still working for higher numbers. For this purpose, 200000 lists with as many elements as the size of the sample we wanted to simulate were generated at random. As the Spearman coefficient only takes into account the ranks, the range in which these numbers were generated was irrelevant as far as it allowed for the avoidance of a lot of repetitions at random. As data from GEO in most of cases ranged from -5 to 5 with three decimals, we chose a range between 0 and 10000, to give the random results approximately the same chance to be repeated as in the original model. The statistical test we perform in this work is applied on the randomly generated lists and p-values are obtained for sample sizes of 4, 7, 10, 20, 50, 70, 100 and 150, which comprise previously simulated methods and also the bigger sample sizes we are studying.

To evaluate the quality of this method, we use the definition of p-value, which is the probability of obtaining a result equal to or "more extreme" than what was actually observed, when the null hypothesis is true. Here, the random generated lists work as a null hypothesis. So, if the method is working correctly, with a p-value of 0.05 or lower, there should be only a 5% of the data, with a p-value of 0.1 or lower, 10% of data, and so on. Because of this, we expect a diagonal straight line when the method is working perfectly, where under a p-value is always its corresponding percentage of data. This can be seen in figure I.1

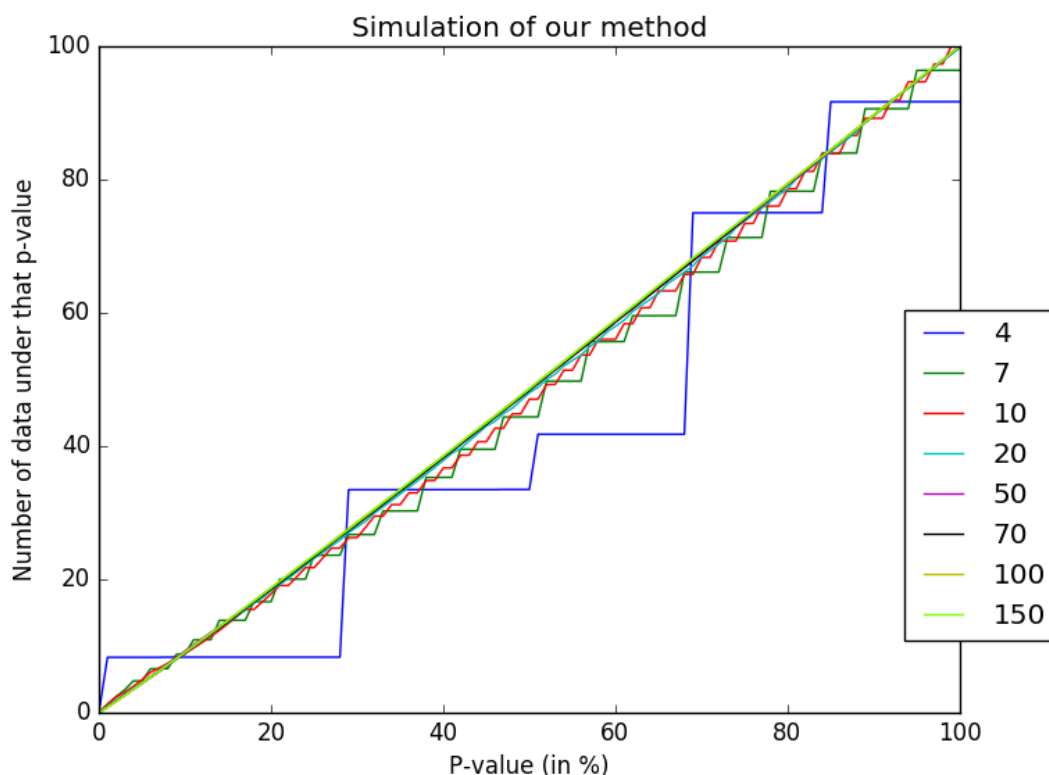


Figure I.1. P-value vs data under that value. On the legend, number of elements in the randomly generated lists. The optimal result is a diagonal straight line going from (0, 0) to (100,100). P-value and number of data are represented as a percentage, so that the slope of the line should be 1. Here, a tendency can be seen to adjust better the higher number of elements in the list, even with a sample number higher than 50. Also, some discretization problems can be observed at lower sample sizes (4 and 7). As there are few numbers, the possible combinations are reduced, so the number of values the result can take is also lower. This can affect the results when calculating FDRs. However, we don't have this problem, as our samples are bigger in all cases except the one we discarded.

To get a better look at the goodness of our method, figure I.2 has been developed. In this figure, we show the deviation of the results obtained from the ones we expected. Deviation is calculated as the percentage of data under a p-value minus that p-value in percentage.

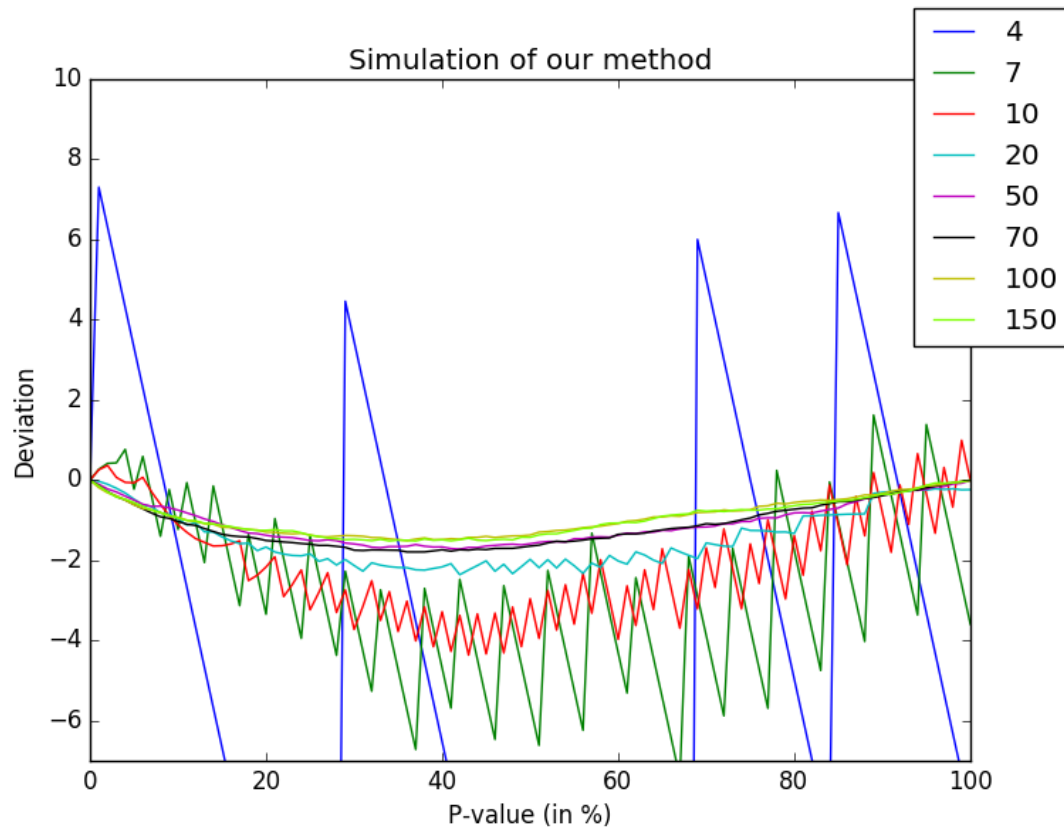


Figure I.2. P-value vs deviation. On the legend, number of elements in the randomly generated lists. Here, the optimal result would be a horizontal line on deviation 0.

This figure shows a tendency to smoothen the deviations with a higher size of the sample. However, a curve can be observed, with a minimum around p-value of 40 (in percentage). However, the interesting part for most of studies is the one going from 0 to 5 in this graph, as the most common p-value is 0.05 for most of the studies. However, this figure shows that the smaller the p-value, the smaller the deviation for almost all sample sizes, so choosing a FDR that selects p-values under 0.004 (see appendix C) seems to be a good idea for reducing deviation in our results.